

1    tgagggccc atgagggcc tgtgtgcgc cccactcctg ctccacttgc tgctggccc  
61   gctgctgctc acggcccg cggtggacgc tggctgtgc tgtcagtatc accgggttt gtgacaagga.  
121   ctccccatgt ggtggaggca ttggggaaac atggggaaac tggggacag ctggccatcca ctgactcgta aaaacaattt  
181   ttgcacacct atggggaaac tggggaaac agggggatgc atcacacttg cccatgtctg ccaggcttgc cctgtttacg  
241   tggaaatggg aggcaaggaa gaagaaaagg gaagagaagg aaaaggaaaa agggggttcc  
301   attttttggg cggaggatgc atcacacttg cccatgtctg ccaggcttgc cctgtttacg  
361   gacttcattt aaccgattta ttgttttagc cccaaaggtaa tcgctctggg gtggaaacca  
421   aatgtga

## FIGURE 1

M R S L C C A P L L L L I P P L I I T P R A G D A A V I T G A C D K D S Q C G G M C C A V S I W V K S I R I C T  
P M G K I I G D S C H P L T R K I N N F G N G R Q E R R K R K R S K R K K E V P F F G R R M H I I T C P C L P G L A C L R T  
S F N R F I C L A Q K

**FIGURE 2**

1   ttagggcc atgaggagcc tttgtctgcgc cccactcctg ctccctttgc tgctgccccc  
61   gaggggccca tgaggaggcct gtgctgcgc ccactcctgc tcctttgtct gctgccccc  
121   ctgctgctca cgccccgcgc tggggacgcc gccgtgtatca cggggcttg tgacaaggac  
181   tcccaatgtg gtggaggcat ttgttgtgtct gtcagtatct gggtcaaggataaaggatt  
241   tgcacaccta tggccaaact gggagacagg tgccatccac tgactcgtaa agttccattt  
301   tttggggaga ggtatgcatca cacttgccca tgtctgcag gcttggcctg tttagggact  
361   tcatttaacc gatttatttg tttagccaa aagtaatgcg tctggatgt aaaccaaatg  
421   tga

### FIGURE 3

MRSLLCCAPLILPPLIITPRAGDAAVITGACCDKDSQCGGGMCCAVSIWVKSIRICT  
PMGKLGDSCCHPLTRKVPPFGRRMHHTCPCLPGLACLRTSFNRFICLAQK

**FIGURE 4**

1 cggacgcgtg ggccgtccccct aaccgccacc gcgtccccgg gacgcccatgg gggaccgcgg  
 61 ctgtgcccccg ctactgctac ttctgtctgt accgctgtctg ttcacacccgc cggccggggaa  
 121 tgcccggtc atcaccgggg cttgcgacaa ggactcttag gatctgcaca cctatggcc aagtggggaa  
 181 tgctgtcaatc atctgggtta agagcataag gatctgcaca cctatggcc aagtggggaa  
 241 cagctgcac cccctgtactc ggaaagtttcc atttgggggg cgaggaggatgc accacacctg  
 301 cccctgcctg ccaggcttg cggttttaag gacttcttcc aaccggttta ttgtcttggc  
 361 ccggaaatga tcactctgaa gttggaaactt gaaatgcgc ctcgcgtgc acaaatgtccg  
 421 tcgagtccta ctgttaatttggccaaacttcc agaataactcc agaaagaat gttctccccc  
 481 ttcccttgact ttccaagtaa cgtttctatc ttgtttttttt gaagttggcattttttttt  
 541 ttttttcc ttcccttga ggaaagtttt gatttttggg gagatttata gaggactttc  
 601 tgacatggct tctcatcc ctgtttatgt ttgccttga catttttggaa tgccaaataaac  
 661 aactgtttc acaaataaggaa gaataaggagg gaaacaatctg ttgcagaaaac ttcccttttg  
 721 cctttggccc actcgccccg cccgcggccg ccccgccctg cccatgcga gacagacaca  
 781 cccttactt tcaaaggactc tgatgtatctt cacccttactg tagcattgtg gtttctaca  
 841 cttcccccgg ttgtctgggtgg acccactgtgg gaggctcaga gagcttagcac tgtacagggt  
 901 tgaaccaggat ccccaaggca gctcatgtgg ggccggacgtt gggaggcgctc caggaacttt  
 961 cctgcaccca tctggcccac tggctttcag ttctgtctgtt taactgggg gaggacaaaa  
 1021 ttaacggggac cctgaaaggaa cctggcccg ttatcttagat ttgttttaagt aaagacatt  
 1081 ttctccttgtt tggtggaaat tacatgtctt ttctttttttt atctgaagttttttt  
 1141 ttctttaagt ctcttttgttgg gagacatttt aaagaacgcgc actcgaggaa gcattgattt  
 1201 tcatytggca tgacaggagt catcatttttta aaaaatcggt gttaagttat aatttaaact  
 1261 ttattttgtaa cccaaaggty taatgtaaat ggattttccctg atatcctgttgg atttgtactg  
 1321 gatatcaatat tttatgtt

**FIGURE 5**

MGDPRCAPLLLLLLPLLFTPPAGDAAVITGACDKDSQCGGGMCCAVSIWVKSIRICTP  
MGQVGDSSCHPLTRKVPPFWGRRMHHTCPCLPGLACLRTSFNRFICLARK

**FIGURE 6**

|              |            |   |     |
|--------------|------------|---|-----|
| <b>Human</b> | <b>BV8</b> | MRSILCCAPILLLPPPLLTPRAGDAAVITGACCDKDSQCGGMCCAVSI                    | 50  |
| <b>Mouse</b> | <b>Bv8</b> | <u>MGDP</u> RCAPI <del>LL</del> PPPLLTPRAGDAAVITGACCDKDSQCGGMCCAVSI |     |
| <hr/>        |            |   |     |
| <b>Human</b> | <b>BV8</b> | WVKSIRICTPMGKLGDSCHPPLTRKNNHGNNGRQEERRRKRSKRKKEVPFF-G               | 100 |
| <b>Mouse</b> | <b>Bv8</b> | WVKSIRICTPMGQVGDSCHPPLTRKSEVANGRQEERRPAKRRRKKEVVPPFWG               |     |
| <hr/>        |            |   |     |
| <b>Human</b> | <b>BV8</b> | RRMHHTCPCLPGIACLRTSFNRFICLQK  | 129 |
| <b>Mouse</b> | <b>Bv8</b> | RRMHHTCPCLPGIACLRTSFNRFICLARK                                       |     |

**FIGURE 7**

1 tggcctcccc agcttgcagg gcacaaaggct gaggggagg aaggcaggagg catctaaggca ggcagggttt  
 71 tggcttcacc ccaagtgacc atgaggaggatg ccacgcgagtc ctcaatcatg ctctccatg taactgtgtc  
 141 tgactgtgt gtgatcacag gggccctgtga gcccggatgtc cagttgggg cagggacccatg ctgtggccatc  
 211 agccctgtggc ttcgagggtct gcggatgtgc accccgcgtgg ggccggaaagg cgaggaggatgc caccggcca  
 281 gccacaagggt ccccttcttc agaaaacgca agcaccacac ctgtcccttgc ttgcccAACCAACC tgctgtgctc  
 351 caggttcccg gacggcagggt accgctgtctc catggacttg aagaacatca atttttaggc gcttggctgg  
 421 tctcaggata cccaccatcc ttttccttgcag cacagccctgg atttttatTTT ctgcccattgaa acccaggctcc  
 491 catgactctc ccaggcccta cactgactac cctgtatctc ctgtcttagt acgcacatATgcacacaggc  
 561 agacatacc cccatcatga catggtcccc aggctggccc aggctggcct gaggatgtca cagctttaggg ctgtgggtgtg  
 631 aaagggtggcc agcctggttc tcttccctgc tcaggctgtcc tcaggctgtgg agagagggtgg taaatggcag aaaggacatt  
 701 ccccccctcccc tccccagggtt acctgtcttc ttccctgggc cctggccctc tccccacatg tatccctcggt  
 771 tctgaatttag acatccctgg gcacaggctc ttgggtgtcat tgctcagagt cccagggtctt ggcctgacc  
 841 tcaggccctt cacgttaggt ctgtgaggac caattttgtgg gtatgttcatc ttccctcgat tggttaactc  
 911 cttagttca gaccacagac tcaaggattgg ctcttcccg agggcaggac acagtcaccc caaggcagggt  
 981 gtagggaggcc cagggaggcc aatcaggcccc ctgaagactc tggtcccaagt cagctgtgg ctgtggcc  
 1051 gtgaccctgtg accttctgtcc agaatttgtca tgcctctgtgg gcccctctt accacacttt accagttaac  
 1121 cactgaaggcc cccaaattccc acagctttc cattaaaaatg caaatgggtgg tggttcaatc taatctgata  
 1191 ttgacatatt agaaggcaat taggtgttt ctttaaaacaa ctctttccaa aggttcagcc ctgagaggcag  
 1261 gtttgtact ttgaggaggc cagtcctctg tccagatgggg ggtggggagg agggacagg agcaggcc  
 1331 gggtgtggaaag gggcaactgtatcagacccagg gaggcaacta cacaccaaca tgctggctt agaataaaag  
 1401 caccaactgtaaaaaa.

## FIGURE 8

Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Val Thr Val Ser  
20 Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly Ala  
40 Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met Cys Thr  
60 Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Val Pro  
70 Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu Pro Asn Leu Leu  
90 Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn  
105 Ile Asn Phe

Figure 9

1    GAA GTG AGG GGT ACC AAA GTA GAC TGT GTT TGT CGT CAC CTC AAG TGA TC

51    ATG AGA GGC GCT GTG CAT ATC TTC ATC ATG CTC CTT CTA GCA ACG GCG TCC  
M    R    G    A    V    H    I    F    I    M    L    L    A    T    A    S

102    GAC TGT GCG GTC ATC ACA GGG GCC TGT GAA CGA GAT ATC CAG TGT GGG GCC  
D    C    A    V    I    T    G    A    C    E    R    D    I    Q    C    G    A

153    GGC ACC TGC TGC GCT ATC AGT CTG TGG CTG CGG GGC CTG CGG TTG TGT ACC  
G    T    C    C    A    I    S    L    W    L    R    G    L    R    L    C    T

204    CCA CTG GGG CGT GAA GGA GAG GAG TGC CAC CCA GGA AGC CAC AAG ATC CCC  
P    L    G    R    E    G    E    E    C    H    P    G    S    H    K    I    P

255    TTC TTG AGG AAA CGC CAA CAC CAT ACC TGT CCC TGC TCA CCC AGC CTG CTG  
F    L    R    K    R    Q    H    H    T    C    P    C    S    P    S    L    L

306    TGC TCC AGG TTC CCG GAC GGC AGG TAC CGC TGC TTC CGG GAC TTG AAG AAT  
C    S    R    F    P    D    G    R    Y    R    C    F    R    D    L    K    N

357    GCC AAC TTT TAGTTTGACTCTGTCTGGACTCTGGCTGACTGGTGAACCTCTTGTTACACCT  
A    N    F    \*

GTGTGATTAGCTCCCTGCAACTCGCCATTCCCACATCTTGTCCGTATGTGCAGACAGGCAGACC  
TTCGCTATGGAATAGTTCACCAAGGGTGCAGAGGGAGTTCTGTGGCCTTGAGAAGTGGCCAGCCCC  
ACCTTCCTGGCTCAAGACTGCCTGAAGTTGTGACAGTGTGGCCCTTCTCAGTTGCCCTGCCCTCCTG  
CATGTGGCCTTCTTCTAAACACACCTTCTGGGCACITGGCCATGGATGCACCAACTAAATCAACA  
GGTCTGTGGGGATGATCAACTTCTCCATTTTCTTATTGACTGGCTTCCATAATTAAAGG  
ACTGT

**Figure 10**

|        |         |            |            |             |            |                   |
|--------|---------|------------|------------|-------------|------------|-------------------|
| Human  | EG-VEGF | MRGATRVSIM | LLLTVSDCA  | VITGACERDV  | QCGAGTCCAI | SLWLRGLRMC        |
| Murine | EG-VEGF | MRGAVHIFIM | LLIATASDCA | VITGACERDI  | QCGAGTCCAI | SLWLRGIRIC        |
|        |         |            |            |             |            |                   |
| Human  | EG-VEGF | TPLGREGEEC | HPGSHKVPFF | RKPKHHITCPC | LPNLLCSRFP | DGRYRCWSMDL KNINF |
| Murine | EG-VEGF | TPLGREGEEC | HPGSHKIPFL | RKRQHHITCPC | SPSLLCSRFP | DGRYRCFRDL KNANF  |

**Figure 11**

|       |           |     |  |
|-------|-----------|-----|--|
| Human | Bv8       | 28  | AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCPIPLTRKVFF  |
|       |           | 20  |  |
| Human | EG-VEGF   |     | AVITGACERDVQCGAGTCICAISLWLRLGILRMCTPLGREGECHPGSHKVPF |
|       |           |     |  |
| Human | Bv8       | 78  |  |
|       |           | 108 | FGRRMHHTCPCLPGLACIERTSFNRIFICLAQK                    |
|       |           | 70  |  |
| Human | EG - VEGF |     | FRKRKHHTCPCLPNLLCSRFPDGRYRCMSMDLKNINF                |
|       |           |     | 105  |

## FIGURE 12

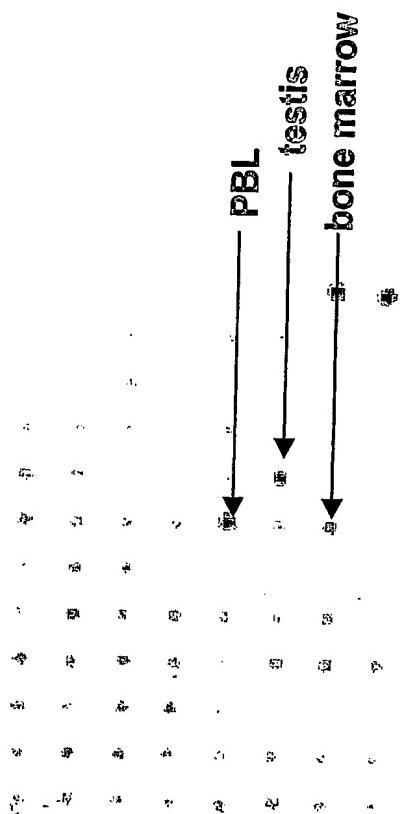


FIGURE 13

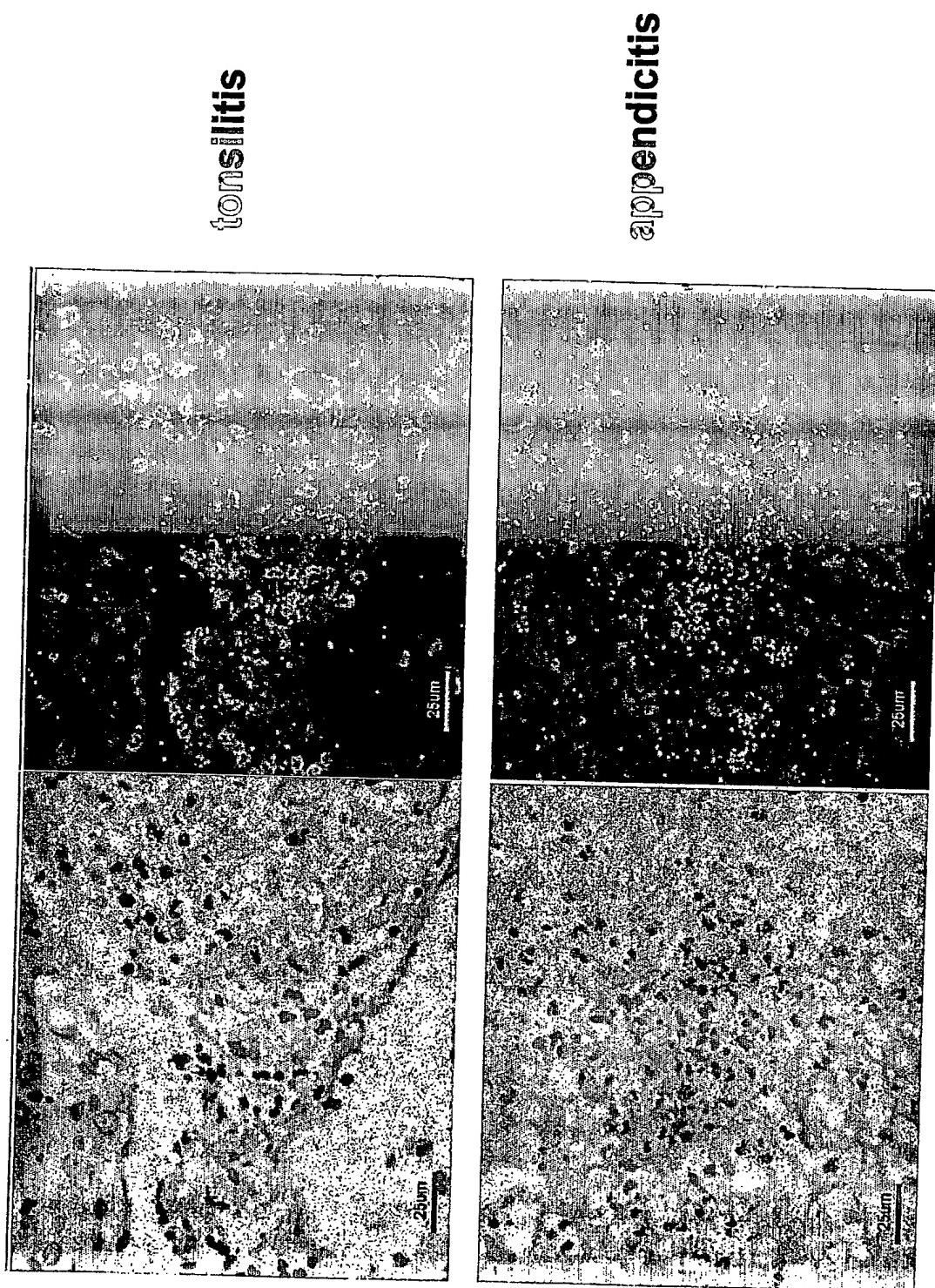
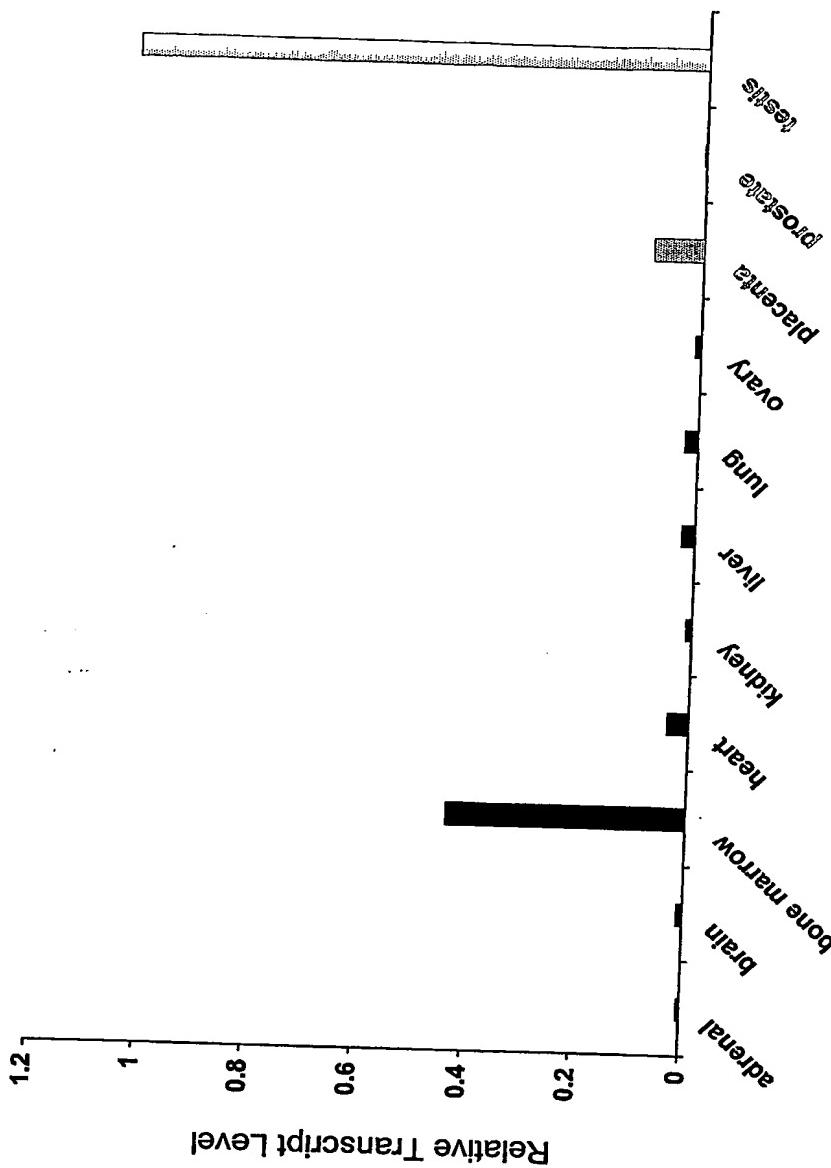


FIGURE 14



**FIGURE 15A**

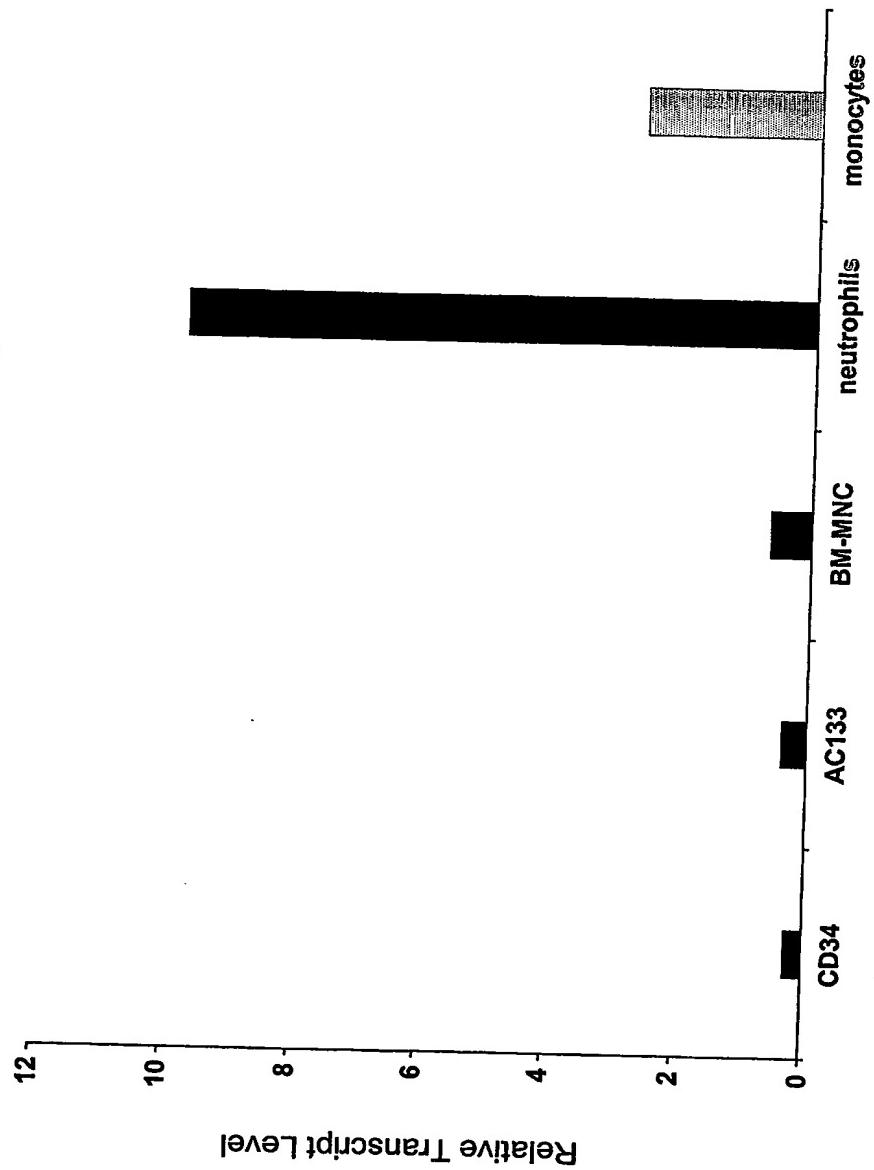


FIGURE 15B

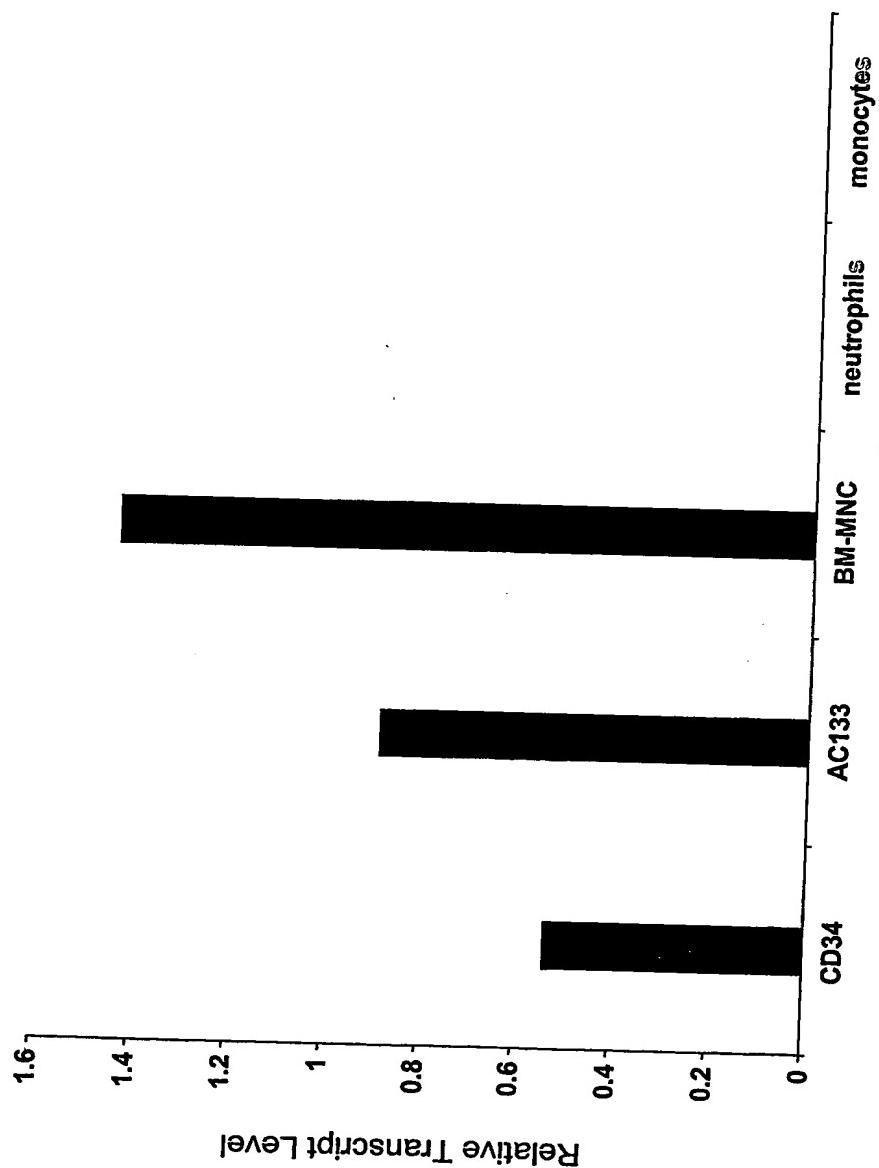


FIGURE 15C

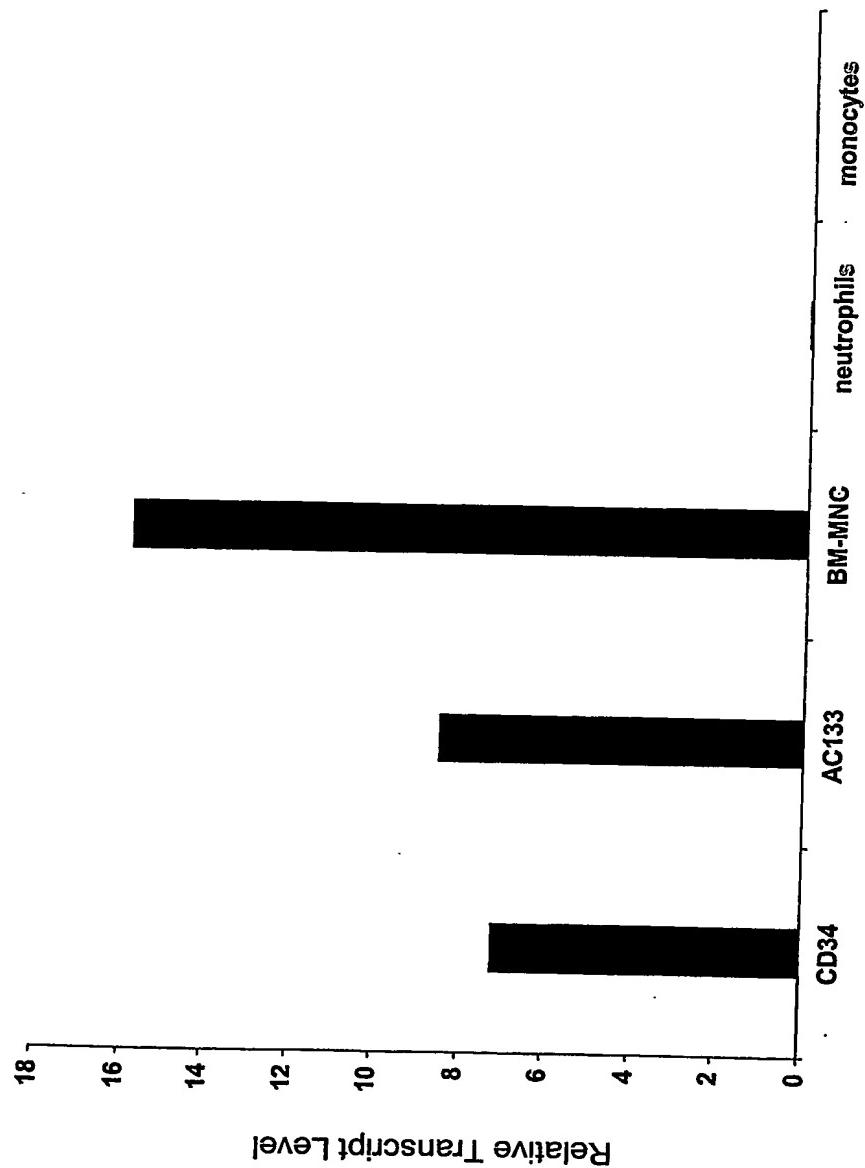
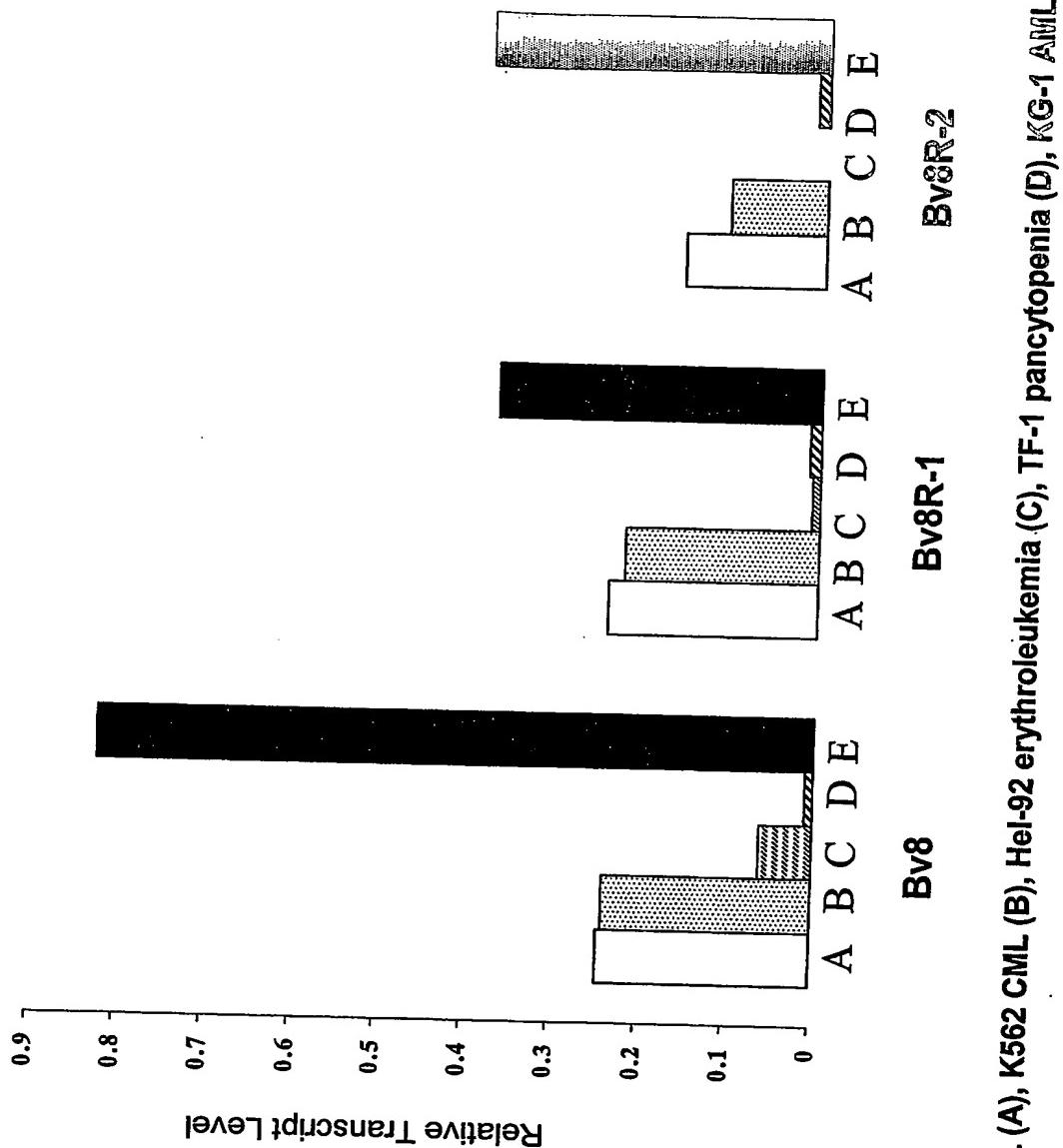
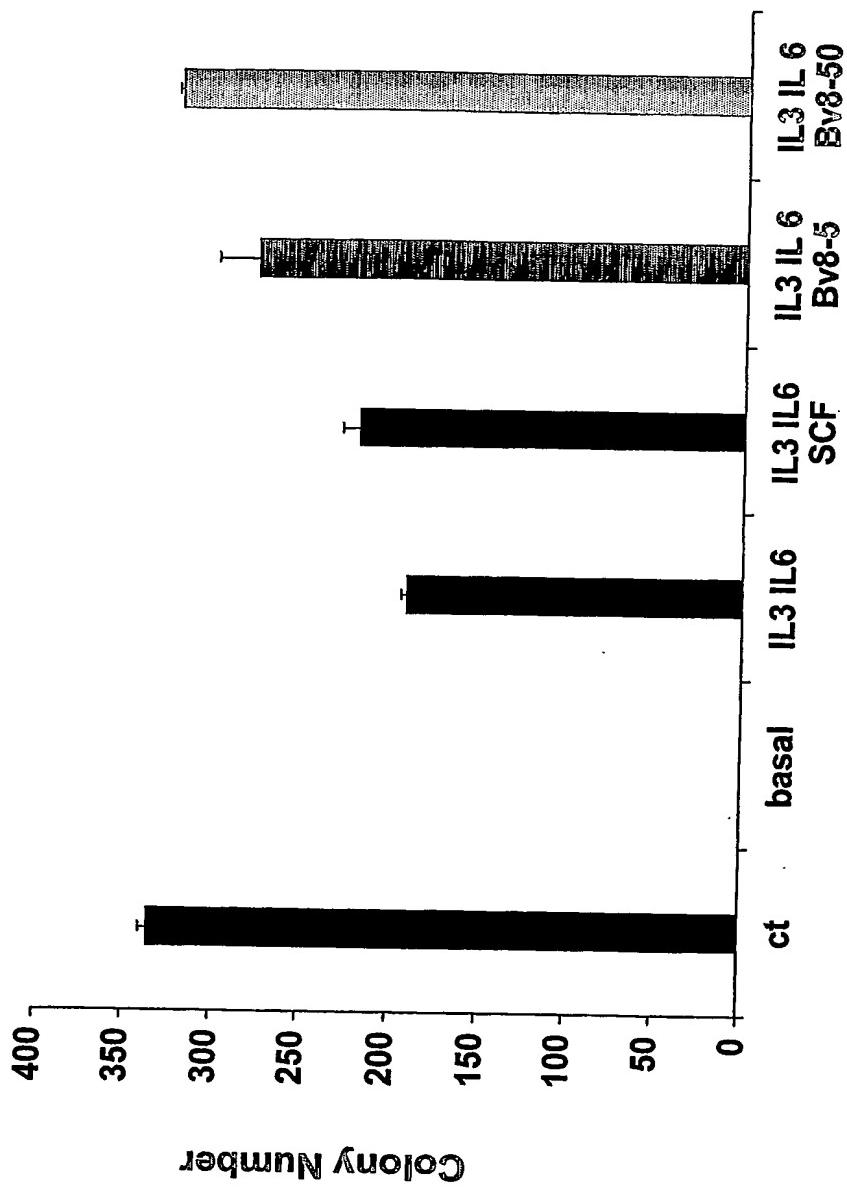


FIGURE 15D



**FIGURE 16**

HL60 CML (A), K562 CML (B), HeLa-92 erythroleukemia (C), TF-1 pancytopenia (D), KG-1 AML (E)



**FIGURE 17A**

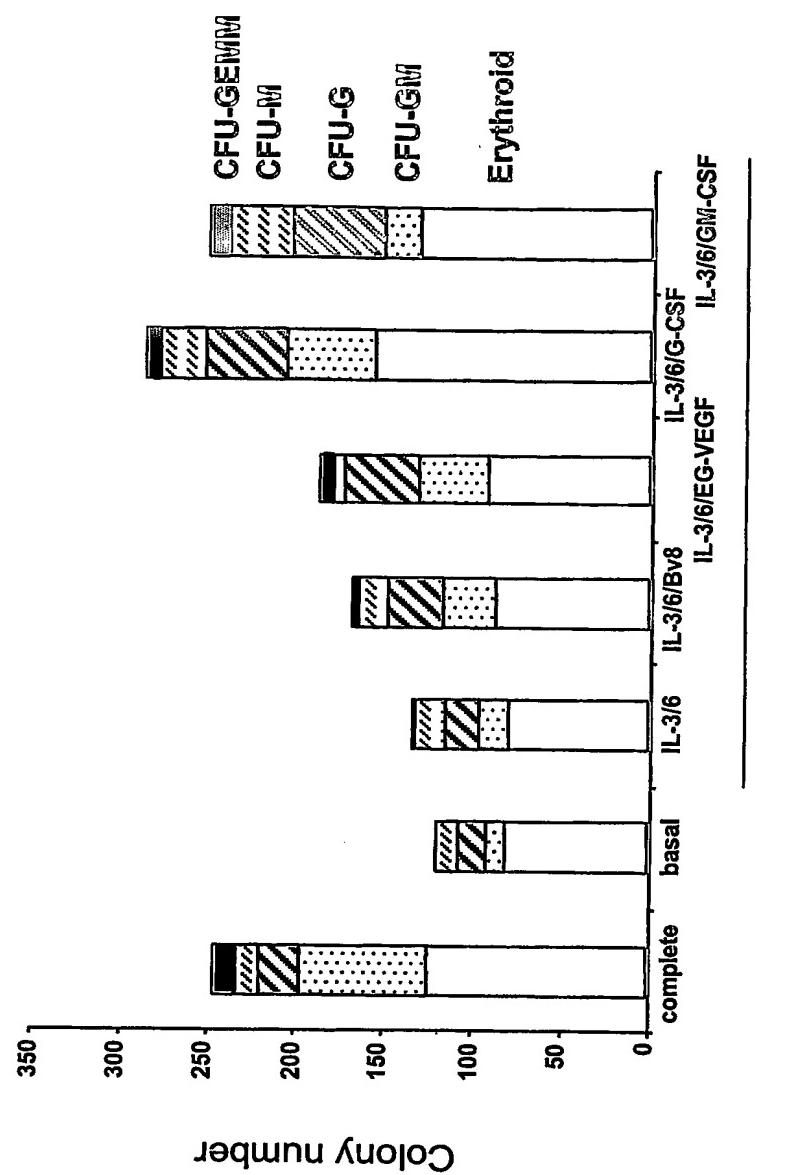


FIGURE 17B

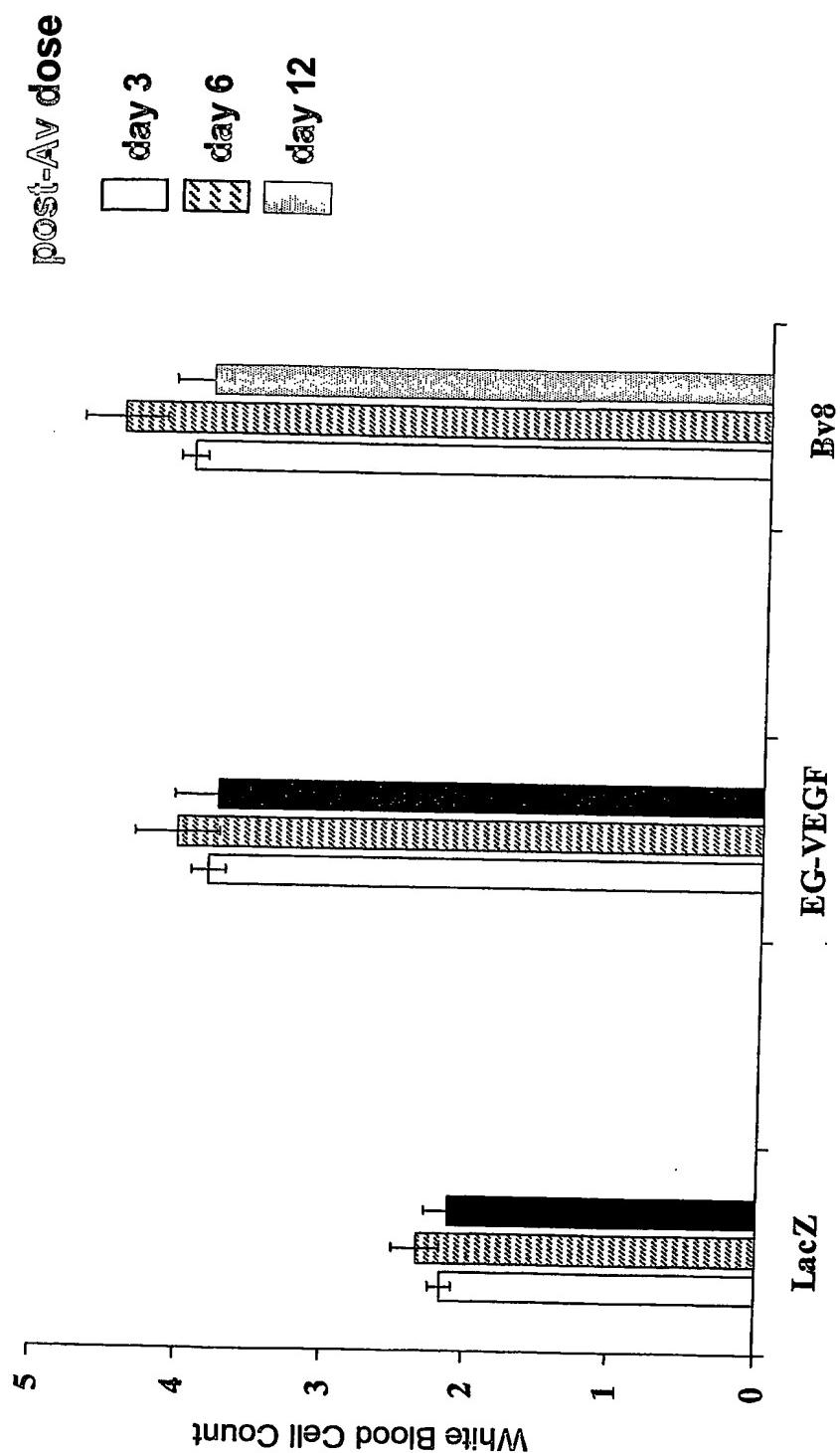


FIGURE 18

Figure 19A

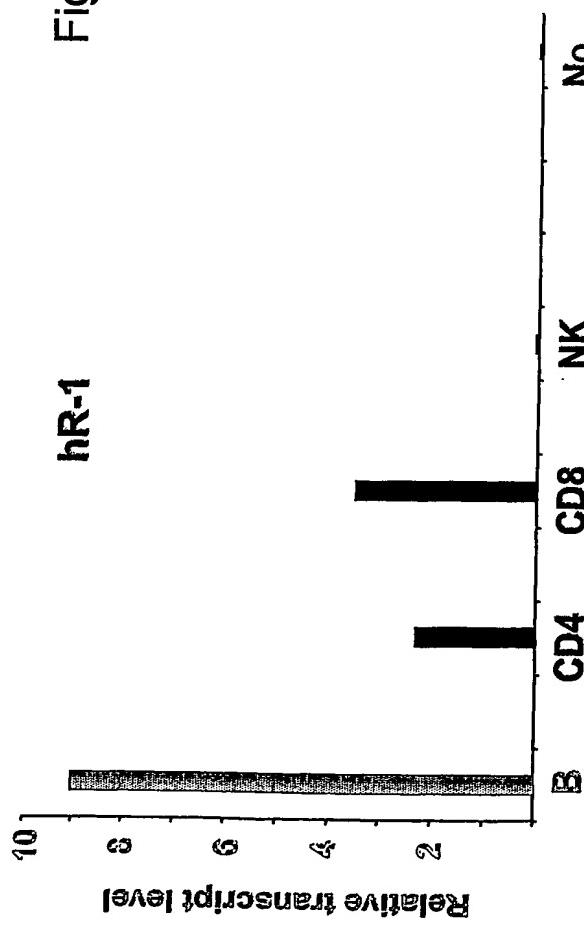
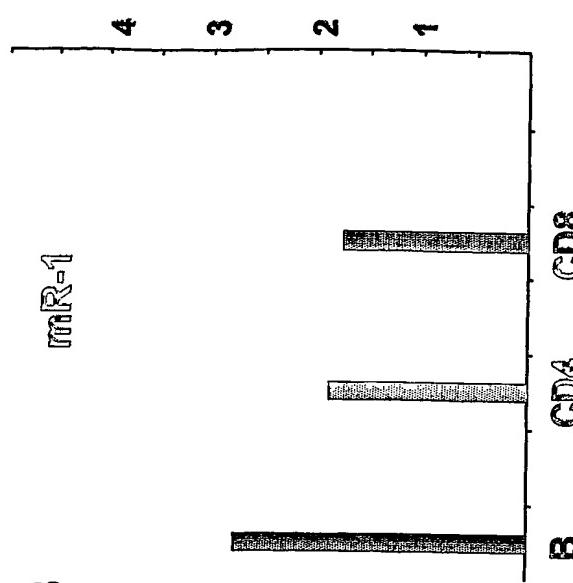


Figure 19B



miR-1

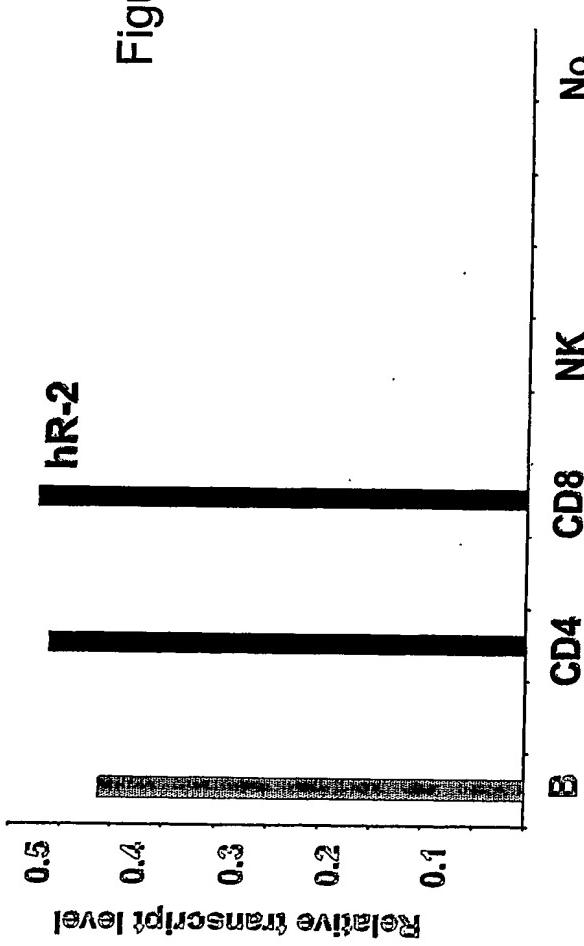
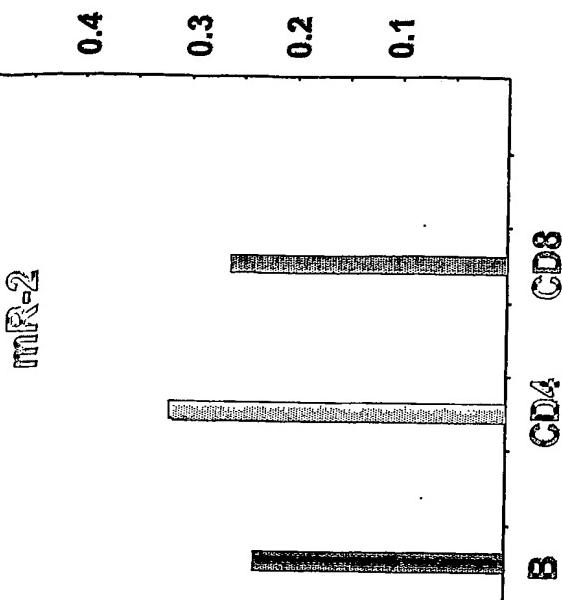


Figure 19C

hR-2



miR-2

miR-1

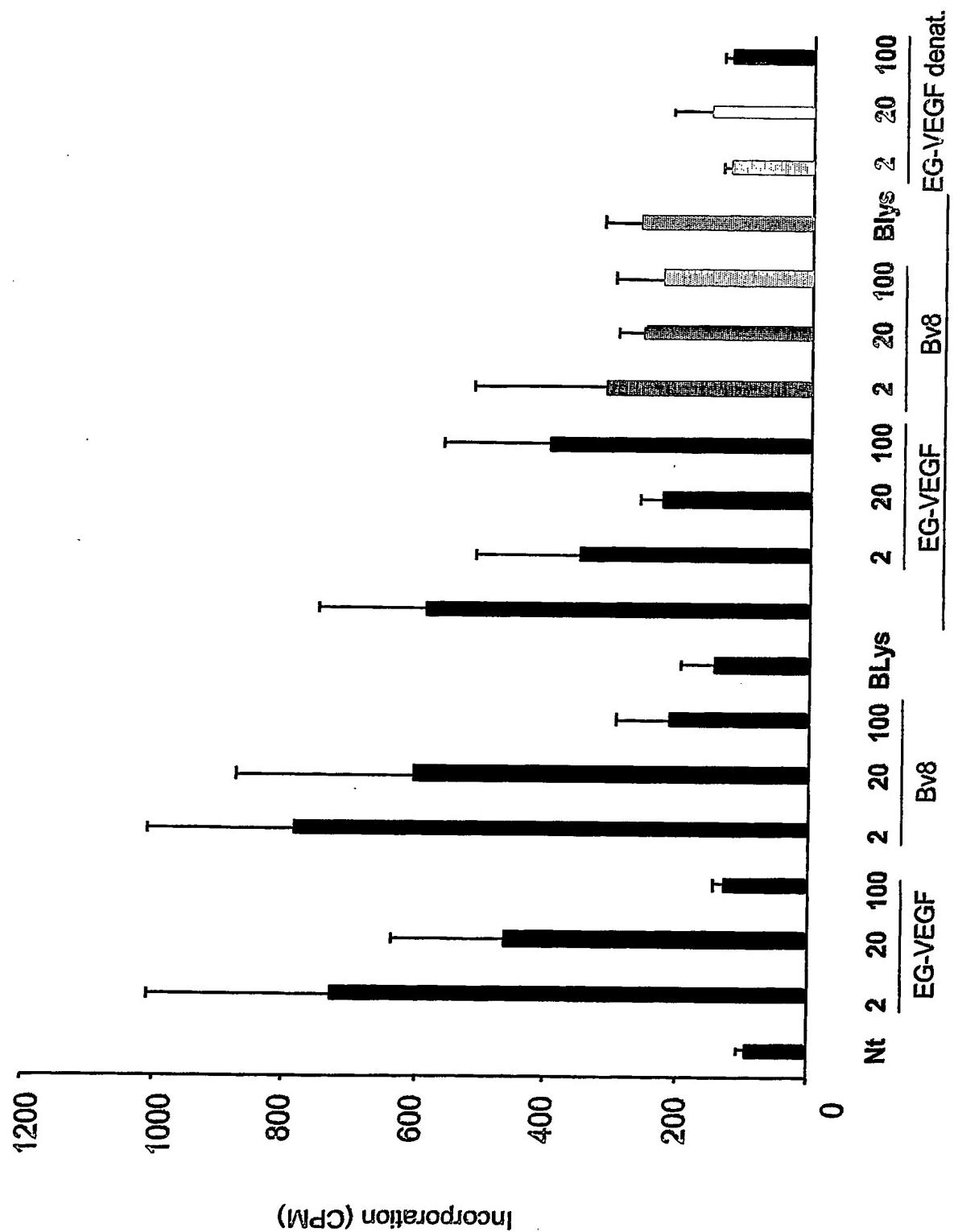


Figure 20 +  $\alpha$ -IgM

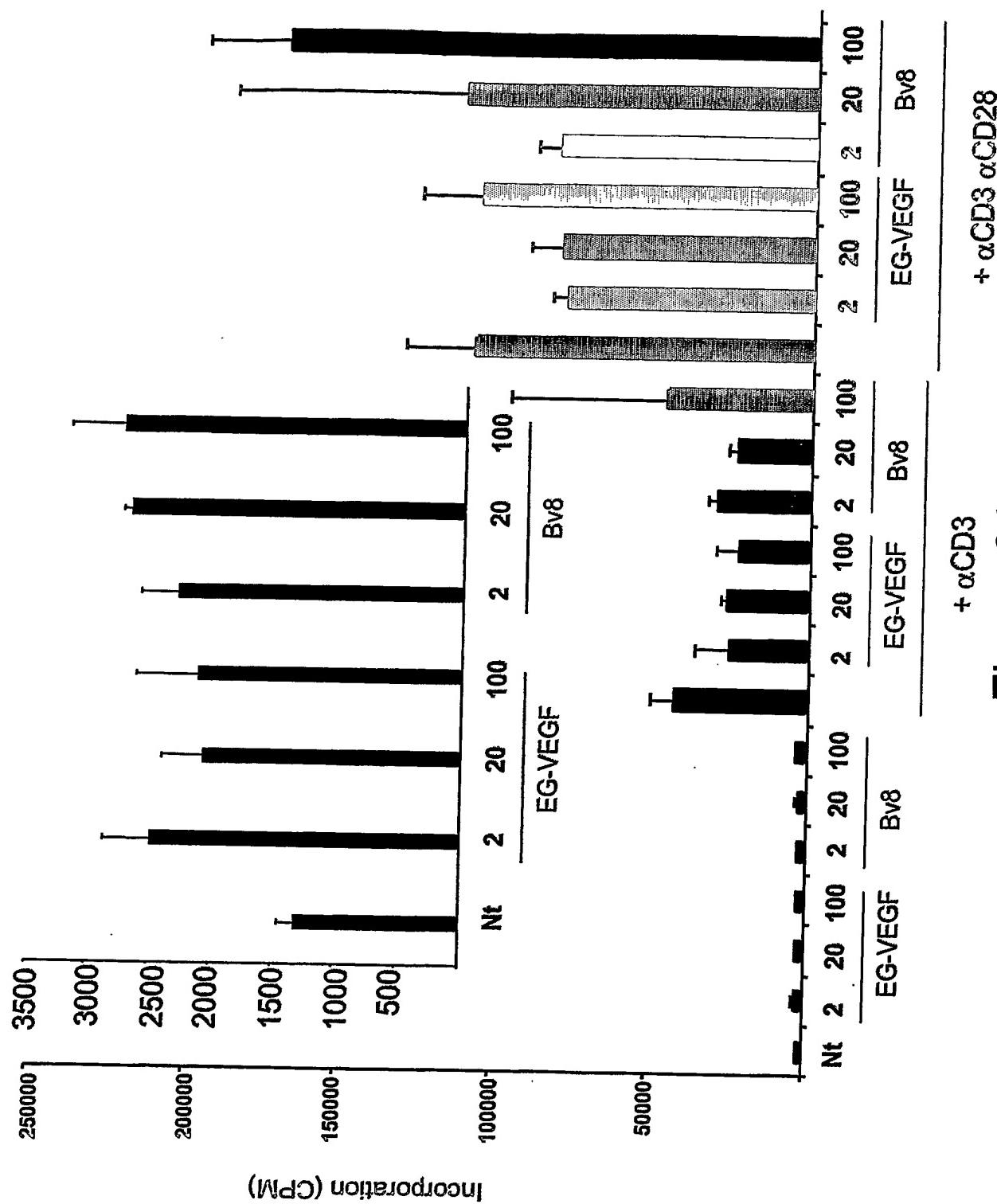
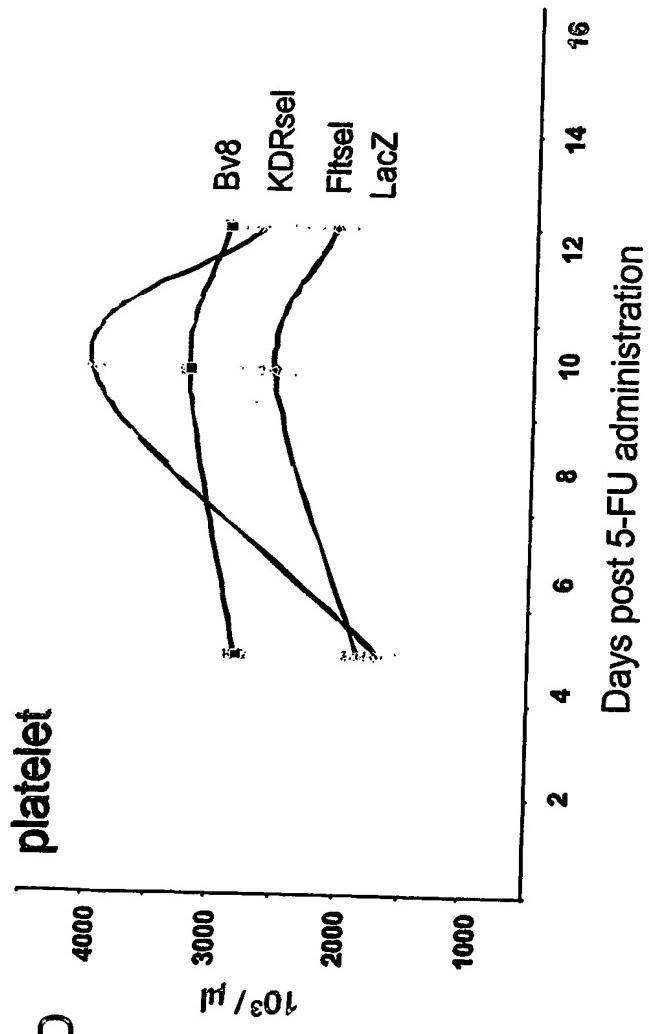
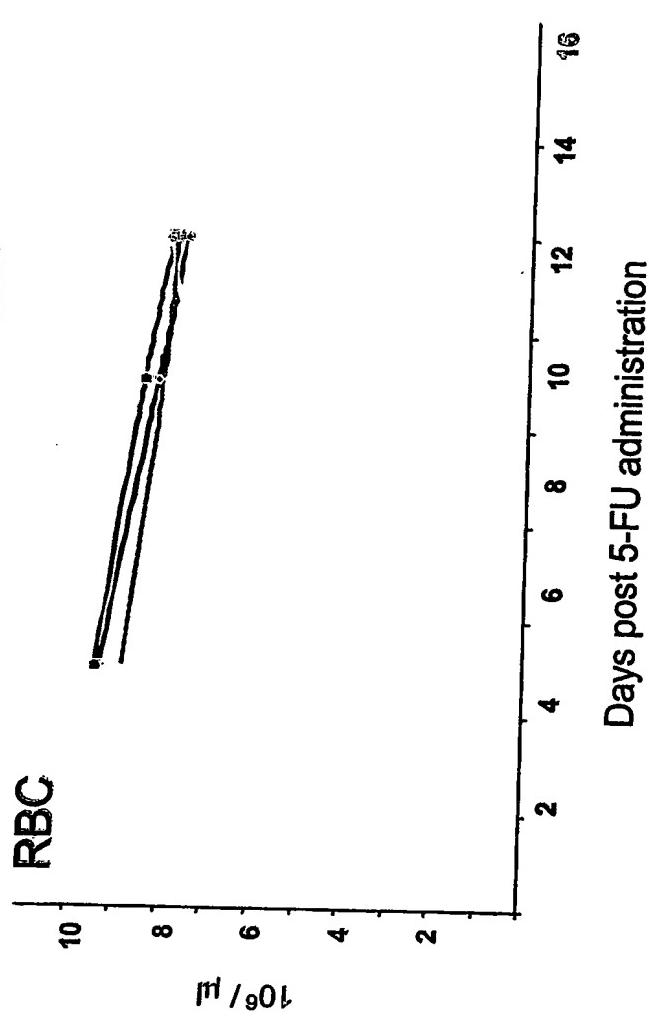


Figure 21

**Figure 23D****Figure 23E**

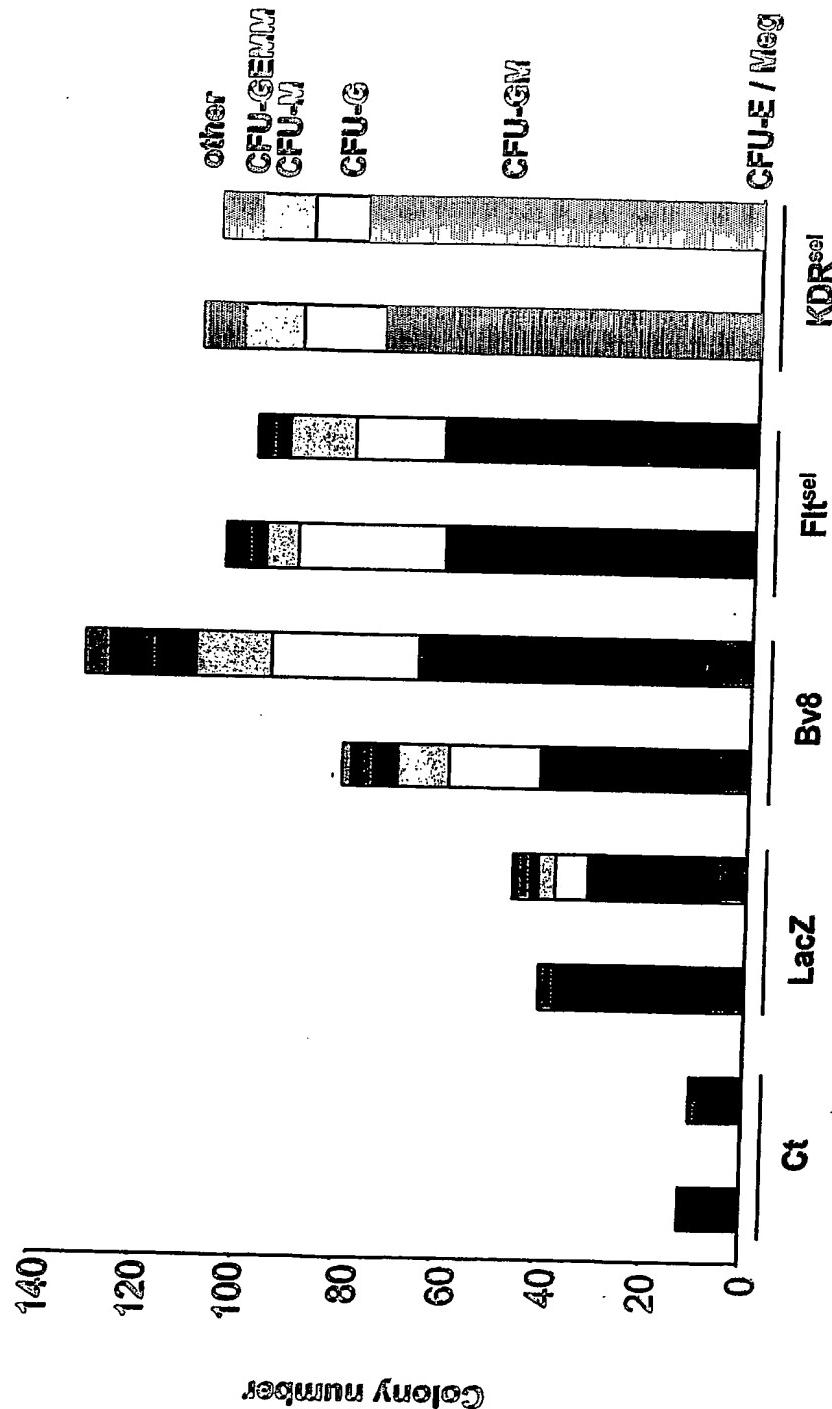


Figure 24